

BEST AVAILABLE COPY

Query= SEQ ID NO:1  
(3963 letters)

Sequences producing significant alignments:

AC024258.9.1.160658  
AL512429.14.1.11170  
AC016395.5.1.166869

Score E  
(bits) Value

1794 0.0  
1159 0.0  
442 e-121

>AC024258.9.1.160658  
Length = 160658

Score = 1794 bits (904), Expect = 0.0  
Identities = 904/904 (100%)  
Strand = Plus / Plus

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SEP 04 2003

TECH CENTER 1600/2900

Query: 1 atgcaagacgacgacatagaagcttctacttccatatctcagcttctaagagagagctat 60  
|||||  
Sbjct: 110106 atgcaagacgacgacatagaagcttctacttccatatctcagcttctaagagagagctat 110165

Query: 61 ttagctgaaaccagacatcggggaaacaatgagaggagtcgagcggagccctcctccaac 120  
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Sbjct: 110166 ttagctgaaaccagacatcggggaaacaatgagaggagtcgagcggagccctcctccaac 110225

Query: 121 ccttgccatttcggcagtccttctggggccgctgaaggaggcggaggccaagatgacctt 180  
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Sbjct: 110226 ccttgccatttcggcagtccttctggggccgctgaaggaggcggaggccaagatgacctt 110285

Query: 181 ccagatctttcagcctttctgagccaagaagaattagacgaaagtgtcaatttggcaaga 240  
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Sbjct: 110286 ccagatctttcagcctttctgagccaagaagaattagacgaaagtgtcaatttggcaaga 110345

Query: 241 ctggccatcaattacgaccctttggagaaggcagatgaaactcaagctagaaaaacgactt 300  
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Sbjct: 110346 ctggccatcaattacgaccctttggagaaggcagatgaaactcaagctagaaaaacgactt 110405

Query: 301 tctcctgatcagatgaaacactcacctaatttaagttttgagcctaacttctgccaggat 360  
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Sbjct: 110406 tctcctgatcagatgaaacactcacctaatttaagttttgagcctaacttctgccaggat 110465

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Sbjct: 110466 aaccctcgaagtcccaccagctctaaagaaagccccaggaggcaaaaaggccacagtat 110525

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Sbjct: 110526 tgttctgaaaccagtcacaaaaaagtatttttaataaggctgccgacttcattgaagag 110585

Query: 481 ctatcctcccttttcaaataccacagctccaaaaggattagacctcgtgcctgcaaaaac 540  
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Sbjct: 110586 ctatcctcccttttcaaataccacagctccaaaaggattagacctcgtgcctgcaaaaac 110645

Query: 541 cacaagagtaaactggaatctcaaaacaaagttatgcaggaaaacagctccagtttctca 600  
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Sbjct: 110646 cacaagagtaaactggaatctcaaaacaaagttatgcaggaaaacagctccagtttctca 110705

Query: 601 gatctgtcagaaagacgagaaagatcttctgttcccatccctatccctgcggataccagg 660  
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Sbjct: 110706 gatctgtcagaaagacgagaaagatcttctgttcccatccctatccctgcggataccagg 110765

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Sbjct: 110766 gataatgaagtgaatcacgccctggaacagcaggaagccaagaggcgtgaagcggagcag 110825

Query: 721 gctgccagtgaaggcggtggtggagacactacaccagggcttcccttcatctctgtac 780  
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|||||  
Sbjct: 110946 ccagaaggaactcgagtacagttggattgcatagtggtaggaattccaccacctcaagta 111005

Query: 901 aggt 904  
||||  
Sbjct: 111006 aggt 111009

Score = 728 bits (367), Expect = 0.0  
Identities = 372/375 (99%)  
Strand = Plus / Plus

Query: 1599 aggaaatgaggacctcagcaacaacgggtctcttcaactcagccaactcyaccaccaacct 1658  
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Sbjct: 154959 aggaaatgaggacctcagcaacaacgggtctcttcaactcagccaactctaccaccaacct 155018

Query: 1659 ggcagctattgagccacagccctccccaccccaactcagagcctccatctgtggaacaacc 1718  
|||||  
Sbjct: 155019 ggcagctattgagccacagccctccccaccccaactcagagcctccatctgtggaacaacc 155078

Query: 1719 ccccaaaccctcgaggggttctggtgaaccacaatgagccccggtccagctccag 1778  
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Sbjct: 155079 ccccaaaccctcgaggggttctggtgaaccacaatgagccccggtccagctccag 155138

Query: 1779 gattgggcttcgtgtgcacttcaacctgcctgaagatgacaaaggaagtgaagcatcctc 1838  
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Sbjct: 155139 gattgggcttcgtgtgcacttcaacctgcctgaagatgacaaaggaagtgaagcatcctc 155198

Query: 1839 cgaggctggtgtggtgaccaccagacagaccaggccccgattctttscaggagaggttcaa 1898  
|||||  
Sbjct: 155199 cgaggctggtgtggtgaccaccagacagaccaggccccgattctttccaggagaggttcaa 155258

Query: 1899 cggacaggcaacaaaaaccccagagccttctttccccgtgaaagagccccctccagttct 1958  
|||||  
Sbjct: 155259 cggacaggcaacaaaaaccccagagccttctttccccgtgaaagagccccctccagttct 155318

Query: 1959 ggccaaaccctaaact 1973  
|||||  
Sbjct: 155319 ggccaaaccctaaact 155333

Score = 355 bits (179), Expect = 1e-94  
Identities = 179/179 (100%)  
Strand = Plus / Plus

Query: 901 aggtggtactgtgaaggcaaggagcttgaaaattccccagatattcacatcgctccaggca 960  
|||||  
Sbjct: 131605 aggtggtactgtgaaggcaaggagcttgaaaattccccagatattcacatcgctccaggca 131664

Query: 961 ggaaatctgcactcactgaccattgcggaagcctttgaagaggacacaggacgctattcc 1020  
|||||  
Sbjct: 131665 ggaaatctgcactcactgaccattgcggaagcctttgaagaggacacaggacgctattcc 131724

Query: 1021 tgctttgcttctaacaatctatgggacagattcgacttctgctgagatttatatagaagg 1079  
|||||  
Sbjct: 131725 tgctttgcttctaacaatctatgggacagattcgacttctgctgagatttatatagaagg 131783

Score = 286 bits (144), Expect = 9e-74  
Identities = 144/144 (100%)  
Strand = Plus / Plus

Query: 1316 agatgctacaaaatttgtcagcttctgagggtcagctggttgtctttgaatgcagagtaa 1375  
|||||  
Sbjct: 147151 agatgctacaaaatttgtcagcttctgagggtcagctggttgtctttgaatgcagagtaa 147210

Query: 1376 aaggagctccatctcctaaggttgagtggatatagagaagggactttaatagaagattctc 1435  
|||||  
Sbjct: 147211 aaggagctccatctcctaaggttgagtggatatagagaagggactttaatagaagattctc 147270

Query: 1436 cagattttaggattttacagaaaa 1459  
|||||  
Sbjct: 147271 cagattttaggattttacagaaaa 147294

Score = 238 bits (120), Expect = 2e-59  
Identities = 120/120 (100%)  
Strand = Plus / Plus

Query: 1482 agaggagatttgacaccttggtcattgctgaggtgtttgcagaagattctgggtgcttcac 1541  
|||||  
Sbjct: 154367 agaggagatttgacaccttggtcattgctgaggtgtttgcagaagattctgggtgcttcac 154426

Query: 1542 atgtactgcaagcaacaaatacggcacagtgtcaagcattgcacagctgcacgtgagagg 1601  
|||||  
Sbjct: 154427 atgtactgcaagcaacaaatacggcacagtgtcaagcattgcacagctgcacgtgagagg 154486

Score = 230 bits (116), Expect = 5e-57  
Identities = 116/116 (100%)  
Strand = Plus / Plus

Query: 1130 gaatccagaagccaaatgaggtgtcatctcctcccactacctctgcagtcattcctccag 1189  
|||||  
Sbjct: 137019 gaatccagaagccaaatgaggtgtcatctcctcccactacctctgcagtcattcctccag 137078

Query: 1190 cagtaccccaagcccagcatttggtggcccaacctcggtgggaaccatccagcag 1245  
|||||  
Sbjct: 137079 cagtaccccaagcccagcatttggtggcccaacctcggtgggaaccatccagcag 137134

Score = 149 bits (75), Expect = 1e-32  
Identities = 75/75 (100%)  
Strand = Plus / Plus

Query: 1243 cagtgtcagagccccaccaattacttgagggttgatggaaaacctatcattgcagct 1302  
|||||  
Sbjct: 138704 cagtgtcagagccccaccaattacttgagggttgatggaaaacctatcattgcagct 138763

Query: 1303 cctgtgtttacaaag 1317  
|||||  
Sbjct: 138764 cctgtgtttacaaag 138778

Score = 107 bits (54), Expect = 5e-20  
Identities = 54/54 (100%)  
Strand = Plus / Plus

Query: 1077 agggggtttcttcttctgactcagaaggcgaccctaacaaggaagagatgaatcg 1130  
|||||  
Sbjct: 134140 agggggtttcttcttctgactcagaaggcgaccctaacaaggaagagatgaatcg 134193

Score = 48.1 bits (24), Expect = 0.041  
Identities = 24/24 (100%)  
Strand = Plus / Plus

Query: 1460 aacctcgatccatggcagagccag 1483  
|||||  
Sbjct: 150396 aacctcgatccatggcagagccag 150419

>AL512429.14.1.11170  
Length = 11170

Score = 1159 bits (584), Expect = 0.0  
Identities = 588/592 (99%)  
Strand = Plus / Plus

Query: 1974 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 2033  
|||||  
Sbjct: 4075 tgattccactcagttacaacagcttcataaccaagtcttactggaacaacaccaattgca 4134

Query: 2034 aaaccacctccttcattctcctaaggagtttcctttcarcatgactgttttgaactccaa 2093  
|||||  
Sbjct: 4135 aaaccacctccttcattctcctaaggagtttcctttcagcatgactgttttgaactccaa 4194

Query: 2094 tgctccccccagcggtgacaacatccartaagcaggtgaagggtccttcattcacagacgtt 2153  
|||||  
Sbjct: 4195 tgctccccccagcggtgacaacatccagtaagcaggtgaagggtccttcattcacagacgtt 4254

Query: 2154 cagcttggccccggccgaagtatttcttccctccacgaacaccaccgcagcaactgtggc 2213  
|||||  
Sbjct: 4255 cagcttggccccggccgaagtatttcttccctccacgaacaccaccgcagcaactgtggc 4314

Query: 2214 cccttccagctctccggtgttcactttgagcagcactcctcaaactattcagaggacagt 2273  
|||||  
Sbjct: 4315 cccttccagctctccggtgttcactttgagcagcactcctcaaactattcagaggacagt 4374

Query: 2274 gagcaaagaaagcctcttagtgtctcaccctctgtgcaaaccaaatctccaggagggct 2333  
|||||  
Sbjct: 4375 gagcaaagaaagcctcttagtgtctcaccctctgtgcaaaccaaatctccaggagggct 4434

Query: 2334 ttccatccaaaatgagccactcccaccaggcccaacagaacccracaccaccaccattcac 2393  
|||||  
Sbjct: 4435 ttccatccaaaatgagccactcccaccaggcccaacagaacccracaccaccaccattcac 4494

Query: 2394 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 2453  
|||||  
Sbjct: 4495 attttccatccccagcggaaccagtttcagccccgctgtgtgtccccaattcctgtctc 4554

Query: 2454 tcctaccagccggattcagaacccagtggtttcctcagctctgtttctgccttctctccc 2513  
|||||  
Sbjct: 4555 tcctaccagccggattcagaacccagtggtttcctcagctctgtttctgccttctctccc 4614

Query: 2514 tgccatcccacccacaaatgccatgggrgctgcctagaagtgcaccatccatg 2565  
|||||  
Sbjct: 4615 tgccatcccacccacaaatgccatggggctgcctagaagtgcaccatccatg 4666

Score = 278 bits (140), Expect = 2e-71  
Identities = 140/140 (100%)  
Strand = Plus / Plus

Query: 2565 gccatcccagggattagcgaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 2624  
|||||  
Sbjct: 5332 gccatcccagggattagcgaagaaaaatacaaagtctcctcaaccagtgaatgatgataa 5391

Query: 2625 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataacttttcagtga 2684  
|||||  
Sbjct: 5392 cattcgtgaaactaagaacgcagtgattcgagacttggggaaaaaaataacttttcagtga 5451

Query: 2685 tgtcagaccaaaccagcagg 2704  
|||||  
Sbjct: 5452 tgtcagaccaaaccagcagg 5471

>AC016395.5.1.166869  
Length = 166869

Score = 442 bits (223), Expect = e-121  
Identities = 226/227 (99%)  
Strand = Plus / Minus

Query: 2701 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 2760  
|||||  
Sbjct: 157129 caggagtacaaaatttcaagctttgagcagaggctgatgaatgaaatagagtttcgcttg 157070

Query: 2761 gaacgtactcctgttgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 2820  
|||||  
Sbjct: 157069 gaacgtactcctgttgatgaatcagatgatgaaattcaacatgatgagatccccacgggc 157010

Query: 2821 aagtgtattgctcccatctttgacaagagactcaagcacttccgggtcacagaaggctct 2880  
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Sbjct: 157009 aagtgtattgctcccatctttgacaagagactcaagcacttccgggtcacagaaggctct 156950

Query: 2881 ccagtcacattcacctgcaaaattggtgggatacctgttccaaaggt 2927  
|||||  
Sbjct: 156949 ccagttacattcacctgcaaaattggtgggatacctgttccaaaggt 156903

Score = 417 bits (210), Expect = e-113  
Identities = 210/210 (100%)  
Strand = Plus / Minus

Query: 3284 aggtgagtgggtttaccgcccccgagctgacatggctactcaatggccaacctgtgctac 3343  
|||||  
Sbjct: 146665 aggtgagtgggtttaccgcccccgagctgacatggctactcaatggccaacctgtgctac 146606

Query: 3344 cagatgcctcccacaagatgctgggtcagggagaccggagtccactctctgctcattgacc 3403  
|||||  
Sbjct: 146605 cagatgcctcccacaagatgctgggtcagggagaccggagtccactctctgctcattgacc 146546

Query: 3404 cactcactcagcgcgacgcagggacctataagtgcacgctaccaacaaaaccgggcaga 3463  
|||||  
Sbjct: 146545 cactcactcagcgcgacgcagggacctataagtgcacgctaccaacaaaaccgggcaga 146486

Query: 3464 attcttttagtctggagctctctgtagtag 3493  
|||||  
Sbjct: 146485 attcttttagtctggagctctctgtagtag 146456

Score = 339 bits (171), Expect = 6e-90  
Identities = 171/171 (100%)  
Strand = Plus / Minus

Query: 3793 gctcagtggcaccatcagatcccaccgcccattgtctgtccggcccagtgggcagtcgctac 3852  
|||||  
Sbjct: 135746 gctcagtggcaccatcagatcccaccgcccattgtctgtccggcccagtgggcagtcgctac 135687

Query: 3853 ggatctctcaccagtaaaggacttgacataattttctgccttttctccatggaaagcacg 3912  
|||||  
Sbjct: 135686 ggatctctcaccagtaaaggacttgacataattttctgccttttctccatggaaagcacg 135627

Query: 3913 atggtgtattcatgctcttctcggagtgtagtggagagtgatgaacttta 3963  
|||||  
Sbjct: 135626 atggtgtattcatgctcttctcggagtgtagtggagagtgatgaacttta 135576

Score = 333 bits (168), Expect = 4e-88  
Identities = 168/168 (100%)  
Strand = Plus / Minus

Query: 3492 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 3551  
|||||  
Sbjct: 144204 agccaaagaggtgaagaaagcacctgtgatcctggagaaactacagaactgcggtgttcc 144145

Query: 3552 cgaaggccaccccgtagactggagtgccgcgtgataggcatgccccacctgtgttcta 3611  
|||||  
Sbjct: 144144 cgaaggccaccccgtagactggagtgccgcgtgataggcatgccccacctgtgttcta 144085

Query: 3612 ctggaagaaagacaatgagaccatcccttgaccagagagaggatcag 3659  
|||||  
Sbjct: 144084 ctggaagaaagacaatgagaccatcccttgaccagagagaggatcag 144037

Score = 306 bits (154), Expect = 9e-80  
Identities = 158/159 (99%), Gaps = 1/159 (0%)  
Strand = Plus / Minus

Query: 2924 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 2983  
|||||  
Sbjct: 151670 aggtttactggttcaaagatgggaagcagatttctaagagaaatgagcactgcaaaatga 151611

Query: 2984 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 3043  
|||||  
Sbjct: 151610 ggcgagaaggagatgggacatgctctctgcacattgaatccactaccagtgatgacgatg 151551



Query: 3044 gcaactacaccatcatggcagccaacccccagg-ggaga 3081  
|||||  
Sbjct: 151550 gcaactacaccatcatggcagccaacccccaggtggaga 151512

Score = 272 bits (137), Expect = 1e-69  
Identities = 137/137 (100%)  
Strand = Plus / Minus

Query: 3657 cagtatgcaccaggacacaacagggatgcctgccttctcattcagccagccaagaaatc 3716  
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Sbjct: 139264 cagtatgcaccaggacacaacagggatgcctgccttctcattcagccagccaagaaatc 139205

Query: 3717 agacgctggatggtacacgttgtcagccaagaatgaagccggcatcgtgtcgtgcactgc 3776  
|||||  
Sbjct: 139204 agacgctggatggtacacgttgtcagccaagaatgaagccggcatcgtgtcgtgcactgc 139145

Query: 3777 caggctggatatatacg 3793  
|||||  
Sbjct: 139144 caggctggatatatacg 139128

Score = 260 bits (131), Expect = 5e-66  
Identities = 131/131 (100%)  
Strand = Plus / Minus

Query: 3157 aggggaagatcccgagtgcaagaaagagacaaagagcccctacaggaacgctttttccga 3216  
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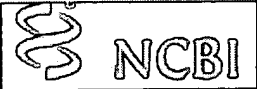
Query: 3217 ccacatttcctgcaggctcctggggatattggtagctcatgaggggcgctctgtcggctg 3276  
|||||  
Sbjct: 148621 ccacatttcctgcaggctcctggggatattggtagctcatgaggggcgctctgtcggctg 148562

Query: 3277 gactgtaaggt 3287  
|||||  
Sbjct: 148561 gactgtaaggt 148551

Score = 173 bits (87), Expect = 1e-39  
Identities = 87/87 (100%)  
Strand = Plus / Minus

Query: 3073 caggggagaaatcagctgttctggccacttgatgggtacaaagtttgccattcgcagtcgg 3132  
|||||  
Sbjct: 150584 caggggagaaatcagctgttctggccacttgatgggtacaaagtttgccattcgcagtcgg 150525

Query: 3133 ctaacctctgctgggtcagtctcacagg 3159  
|||||  
Sbjct: 150524 ctaacctctgctgggtcagtctcacagg 150498



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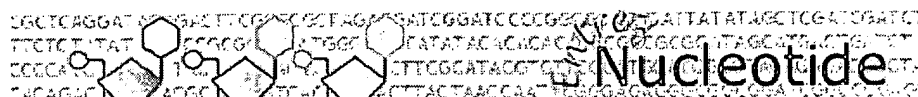
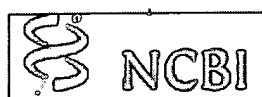
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[Links](#)

LOCUS AC024258 160658 bp DNA linear PRI 14-MAY-2002  
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 ACCESSION AC024258  
 VERSION AC024258.9 GI:20564414  
 KEYWORDS HTG.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 160658)  
 AUTHORS Smith,D.R.  
 TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome  
 Sequence Data  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 160658)  
 AUTHORS Smith,D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (28-FEB-2000) Genome Therapeutics Corporation, 100 Beaver  
 Street, Waltham, MA 02453, USA  
 REFERENCE 3 (bases 1 to 160658)  
 AUTHORS Smith,D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-NOV-2001) Genome Therapeutics Corporation, 100 Beaver  
 Street, Waltham, MA 02453, USA  
 REFERENCE 4 (bases 1 to 160658)  
 AUTHORS Smith,D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-MAY-2002) Genome Therapeutics Corporation, 100 Beaver  
 Street, Waltham, MA 02453, USA  
 COMMENT On May 14, 2002 this sequence version replaced gi:16905139.  
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 ORIGIN

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121 tccttgttcc tacagcagca gaatggatgt tgtattagca ggcataaaaa cattaatctc
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LOCUS AL512429 11170 bp DNA linear PRI 26-OCT-2001

DEFINITION Human DNA sequence from clone RP11-429C3 on chromosome 10, complete sequence.

ACCESSION AL512429

VERSION AL512429.14 GI:16508239

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 11170)

AUTHORS Mashreghi-Mohammadi, M.

TITLE Direct Submission

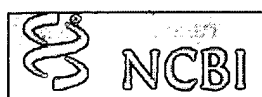
JOURNAL Submitted (26-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Oct 29, 2001 this sequence version replaced gi:15028699. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10> RP11-429C3 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VECTOR: pBACe3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-429C3 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-153K11 is at 9171 in this sequence.



Nucleotide  
 Protein  
 Genome  
 Structure  
 PMC  
 Taxonomy  
 OMIM  
 Bio

Search  for

Limits Preview/Index History Clipboard Details

Display  Show:  Send to  Get Subsequence Fe

1: AC016395. Homo sapiens chro...[gi:20564406]

Links

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 VERSION AC016395.5 GI:20564406  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 166869)  
 AUTHORS Smith,D.R.  
 TITLE Genome Therapeutics Corporation Sequencing Center: Human Genome  
 Sequence Data  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 166869)  
 AUTHORS Smith,D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-NOV-1999) Genome Therapeutics Corporation, 100 Beaver  
 Street, Waltham, MA 02453, USA  
 REFERENCE 3 (bases 1 to 166869)  
 AUTHORS Smith,D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (26-AUG-2000) Genome Therapeutics Corporation, 100 Beaver  
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 AUTHORS Smith,D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-MAY-2002) Genome Therapeutics Corporation, 100 Beaver  
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 COMMENT On May 14, 2002 this sequence version replaced gi:9929646.  
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SEP 02 2003

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